

RAW SEQUENCE LISTING

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Application Serial Number: 09/422,999 A
Source: IFW/6
Date Processed by STIC: 3-22-05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/22/2005

PATENT APPLICATION: US/09/422,999A

TIME: 11:41:00

Input Set : A:\MIT-103.ST25.txt

Output Set: N:\CRF4\03222005\I422999A.raw

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3 <110> APPLICANT: Kawasaki, Hiroaki
4      Graybiel, Ann
5      Housman, David
7 <120> TITLE OF INVENTION: Genes Integrating Signal Transduction Pathways
9 <130> FILE REFERENCE: MIT-103
11 <140> CURRENT APPLICATION NUMBER: US 09/422,999A
12 <141> CURRENT FILING DATE: 1999-10-22
14 <150> PRIOR APPLICATION NUMBER: US 60/105,507
15 <151> PRIOR FILING DATE: 1998-10-23
17 <150> PRIOR APPLICATION NUMBER: US 60/108,685
18 <151> PRIOR FILING DATE: 1998-11-16
20 <160> NUMBER OF SEQ ID NOS: 58
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2250
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (166)..(1989)
34 <400> SEQUENCE: 1
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37 cggggtttgca ttctgaagta aaggacttgg gacaggggta cgaatcgagc actgtggggag      120
39 gctctgagag tgtaacttgg gtctagccca ctggcaccgg cagcc atg gcg agc act      177
40                                     Met Ala Ser Thr
41                                     1
43 ctg gac ctg gac aag ggt tgc acc gtg gag gag ctg ctc cgt ggc tgt      225
44 Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys
45 5                               10                               15                               20
47 atc gaa gcc ttt gat gac tct gga aag gtg cga gat cca cag cta gtg      273
48 Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val
49                               25                               30                               35
51 cgc atg ttt ctc atg atg cac ccc tgg tac ata cct tcc tct cag ctg      321
52 Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu
53                               40                               45                               50
55 gct tcg aaa ctg ctc cac ttc tat cag caa tcc cgg aag gac aac tcc      369
56 Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg Lys Asp Asn Ser
57                               55                               60                               65
59 aat tcc cta cag gtg aaa acc tgt cac ctg gtc agg tac tgg gtc tca      417
60 Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg Tyr Trp Val Ser
61                               70                               75                               80
63 gcc ttc cca gca gag ttc gac ttg aac cca gag ctg gct gaa ccg atc      465
64 Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Pro Ile

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65	85	90	95	100	
67	aag gag ctg aag gct ctg tta gac caa gaa gga aac cgc agg cac agc	513			
68	Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser				
69	105 110 115				
71	agc ctc atc gac atc gag agt gtc ccc acc tac aag tgg aag cgg cag	561			
72	Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln				
73	120 125 130				
75	gtg acc cag cgg aac cct gtg gaa cag aaa aag cgc aag atg tcc ctg	609			
76	Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg Lys Met Ser Leu				
77	135 140 145				
79	ttg ttt gat cac ttg gag cct atg gaa ctg gca gaa cat ctc acc tac	657			
80	Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr				
81	150 155 160				
83	ttg gag tat cgg tcc ttc tgc aag atc ctg ttc cag gac tat cac agc	705			
84	Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser				
85	165 170 175 180				
87	ttt gtg act cat ggc tgc act gta gac aat ccg gtc ctg gag cga ttc	753			
88	Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe				
89	185 190 195				
91	atc tcc ctc ttc aac agt gtc tct cag tgg gtc caa ctc atg atc ctc	801			
92	Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu				
93	200 205 210				
95	agc aag ccc aca gcc acg cag cgg gcg ctg gtc atc aca cat ttc gtg	849			
96	Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile Thr His Phe Val				
97	215 220 225				
99	cat gtg gca gag aag ctg ctg cag ctg cag aac ttc aac acg ttg atg	897			
100	His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met				
101	230 235 240				
103	gcc gtc gtg gga ggc ctg agc cac agc tcc atc tca cgc ctc aag gag	945			
104	Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu				
105	245 250 255 260				
107	acc cac agc cat gtc agc cct gac acc atc aag ctc tgg gaa ggt ctg	993			
108	Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu Trp Glu Gly Leu				
109	265 270 275				
111	aca gaa cta gtg aca gct act ggc aac tac agc aac tac cgg cga agg	1041			
112	Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn Tyr Arg Arg Arg				
113	280 285 290				
115	ctg gcg gcc tgc gtg ggc ttc cgc ttt cct atc ctg ggt gtg cac ctc	1089			
116	Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu				
117	295 300 305				
119	aag gat cta gtg gct ctg cag ctg gct ctg cct gac tgg ctg gac cca	1137			
120	Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp Trp Leu Asp Pro				
121	310 315 320				
123	ggt cgg acc cgg ctc aat gga gcc aag atg agg cag ctt ttc agc att	1185			
124	Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln Leu Phe Ser Ile				
125	325 330 335 340				
127	ctg gag gag ttg gct atg gtg acc agt ctt cga cca cca gtg caa gcc	1233			
128	Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala				
129	345 350 355				

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131 aac ccc gac ctg ctg agt ctg ctc acg gtg tcc ctg gac cag tat cag      1281
132 Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu Asp Gln Tyr Gln
133          360          365          370
135 acg gag gat gag ctg tat cag ctc tct ctg cag cga gag cca cgt tcc      1329
136 Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser
137          375          380          385
139 aag tca tcg ccc acc agc ccc acc agc tgc acc ccg cct ccc cgg ccg      1377
140 Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro Pro Pro Arg Pro
141          390          395          400
143 cct gtg ctg gaa gag tgg acc tca gtt gcc aag cct aag ctg gac caa      1425
144 Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro Lys Leu Asp Gln
145 405          410          415          420
147 gcc ttg gtg gcc gag cac att gag aag atg gtg gag tct gtg ttc cgg      1473
148 Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu Ser Val Phe Arg
149          425          430          435
151 aac ttt gac gtt gat ggg gac ggt cac atc tcc cag gag gag ttc cag      1521
152 Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe Gln
153          440          445          450
155 atc atc cgg ggc aac ttc cct tat ctc agc gcc ttt ggg gac ttg gac      1569
156 Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe Gly Asp Leu Asp
157          455          460          465
159 cag aac cag gat ggc tgc atc agc cgg gag gag atg att tcc tac ttc      1617
160 Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met Ile Ser Tyr Phe
161          470          475          480
163 ctg cgc tcc agc tcc gtg ctg gga ggc cgc atg ggc ttc gta cac aac      1665
164 Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly Phe Val His Asn
165 485          490          495          500
167 ttc cag gag agt aac tcg cta agg ccg gtc gcc tgc cga cac tgc aaa      1713
168 Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His Cys Lys
169          505          510          515
171 gct ctg atc ctg ggc atc tac aag cag ggc ctc aaa tgt aga gct tgt      1761
172 Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg Ala Cys
173          520          525          530
175 ggt gtg aac tgc cac aag cag tgc aaa gac cga ctg tca gtg gaa tgt      1809
176 Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val Glu Cys
177          535          540          545
179 cgc cgc cgc gcc cag agt gtg agc ctg gag ggc tct gca ccc tct ccc      1857
180 Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser Ala Pro Ser Pro
181          550          555          560
183 tca ccc aca cat acc cac cat cgg gcc ttc agc ttc tcc ctg cct cgc      1905
184 Ser Pro Thr His Thr His His Arg Ala Phe Ser Phe Ser Leu Pro Arg
185 565          570          575          580
187 cca ggc agg cgc agc tct cgg cct cca gag atc cgt gaa gag gag gtg      1953
188 Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val
189          585          590          595
191 cag act gtg gaa gat ggt gtg ttc gac atc cac tta taagacgctg      1999
192 Gln Thr Val Glu Asp Gly Val Phe Asp Ile His Leu
193          600          605
195 tgactatcaa ggactcattc ctgccttggga gaaaagactt ggagcagagc agggagccag      2059

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199 aaaaaaggcc agggctggtg tccctaaggt tgtacagact tctgtgaata tttgtatttt 2179
201 ccagatggaa taaaaaggcc cgaataatta acctcgaaaa aaaaaaaaaa aaaaaaaaaa 2239
203 aaaaaaaaaa a 2250
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 608
208 <212> TYPE: PRT
209 <213> ORGANISM: Mus musculus
211 <400> SEQUENCE: 2
213 Met Ala Ser Thr Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu
214 1 5 10 15
217 Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp
218 20 25 30
221 Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro
222 35 40 45
225 Ser Ser Gln Leu Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg
226 50 55 60
229 Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg
230 65 70 75 80
233 Tyr Trp Val Ser Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu
234 85 90 95
237 Ala Glu Pro Ile Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn
238 100 105 110
241 Arg Arg His Ser Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys
242 115 120 125
245 Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg
246 130 135 140
249 Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu
250 145 150 155 160
253 His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln
254 165 170 175
257 Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val
258 180 185 190
261 Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln
262 195 200 205
265 Leu Met Ile Leu Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile
266 210 215 220
269 Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe
270 225 230 235 240
273 Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser
274 245 250 255
277 Arg Leu Lys Glu Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu
278 260 265 270
281 Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn
282 275 280 285
285 Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu
286 290 295 300
289 Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp
290 305 310 315 320

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293 Trp Leu Asp Pro Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln
294           325           330           335
297 Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro
298           340           345           350
301 Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu
302           355           360           365
305 Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg
306           370           375           380
309 Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro
310 385           390           395           400
313 Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro
314           405           410           415
317 Lys Leu Asp Gln Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu
318           420           425           430
321 Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln
322           435           440           445
325 Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe
326           450           455           460
329 Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met
330 465           470           475           480
333 Ile Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly
334           485           490           495
337 Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys
338           500           505           510
341 Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys
342           515           520           525
345 Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu
346           530           535           540
349 Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser
350 545           550           555           560
353 Ala Pro Ser Pro Ser Pro Thr His Thr His Arg Ala Phe Ser Phe
354           565           570           575
357 Ser Leu Pro Arg Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg
358           580           585           590
361 Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val Phe Asp Ile His Leu
362           595           600           605
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366 <211> LENGTH: 2236
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
371 <220> FEATURE:
372 <221> NAME/KEY: CDS
373 <222> LOCATION: (161)..(1987)
375 <400> SEQUENCE: 3
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380 ggagcgcgac ctggggcccag cccaccccgc gccggcgggcc atg gca ggc acc ctg 175
381 Met Ala Gly Thr Leu
382 1 5

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VERIFICATION SUMMARY

DATE: 03/22/2005

PATENT APPLICATION: US/09/422,999A

TIME: 11:41:02

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